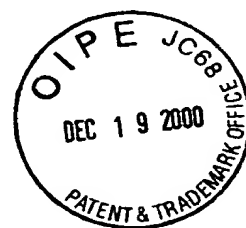


SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: OSUMI Chieko
NOZAKI Jinshi
KIDA Takao
- (ii) TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR
PRODUCING RAFFINOSE, AND TRANSGENIC PLANT
- (iii) NUMBER OF SEQUENCES: 22
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 - (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 - (C) CITY: ARLINGTON
 - (D) STATE: VIRGINIA
 - (E) COUNTRY: USA
 - (F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (vi) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: NORMAN F. OBLON
 - (B) REGISTRATION NUMBER: 24,618
- (vii) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703)-413-3000
 - (B) TELEFAX: (703)-413-2220

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Phe	Gly	Trp	Cys	Thr	Trp	Asp	Ala	Phe	Tyr	Leu	Thr	Val	His	Pro	Gln
1				5					10					15	
Gly	Val	Ile	Glu	Gly	Val	Arg	His	Leu	Val	Asp	Gly	Gly	Cys		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ro Val Ser Val Gly Cys Phe Val Gly Phe Asp Ala Ser Glu Pro Asp
 1 5 10 15
 er Arg His

2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

tyr Asp Gln Asp Gln Met Val Val Val Gln Val Pro Trp Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2517 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: cucumber (Cucumis sativas)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 56..2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAAAAACAAC CCTTCTTTTA GTTTTTTGGG TTTGTTTCTT CTTTCTTCT CACAA ATG	58
Met	
1	
GCT CCT AGT TTT AAA AAT GGT GGC TCC AAC GTA GTT TCA TTT GAT GGC	106
Ala Pro Ser Phe Lys Asn Gly Gly Ser Asn Val Val Ser Phe Asp Gly	
5 10 15	
TTA AAT GAC ATG TCG TCA CCG TTT GCA ATC GAC GGA TCG GAT TTC ACT	154
Leu Asn Asp Met Ser Ser Pro Phe Ala Ile Asp Gly Ser Asp Phe Thr	
20 25 30	
GTG AAC GGT CAT TCG TTT CTG TCC GAT GTT CCT GAG AAC ATT GTT GCT	202
Val Asn Gly His Ser Phe Leu Ser Asp Val Pro Glu Asn Ile Val Ala	
35 40 45	
TCT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT TCG GTT GGT	250
Ser Pro Ser Pro Tyr Thr Ser Ile Asp Lys Ser Pro Val Ser Val Gly	
50 55 60 65	
TGC TTT GTT GGA TTC GAC GCG TCG GAA CCT GAT AGC CGA CAT GTT GTT	298
Cys Phe Val Gly Phe Asp Ala Ser Glu Pro Asp Ser Arg His Val Val	
70 75 80	
TCG ATT GGG AAG CTG AAG GAT ATT CGG TTT ATG AGT ATT TTC AGG TTT	346
Ser Ile Gly Lys Leu Lys Asp Ile Arg Phe Met Ser Ile Phe Arg Phe	

85					90					95						
AG	GTT	TGG	TGG	ACT	ACA	CAC	TGG	GTT	GGT	CGA	AAT	GGT	GGG	GAT	CTT	394
lys	Val	Trp	Trp	Thr	Thr	His	Trp	Val	Gly	Arg	Asn	Gly	Gly	Asp	Leu	
		100					105					110				
AAA	TCG	GAG	ACT	CAG	ATT	GTG	ATC	CTT	GAG	AAG	TCA	GAT	TCT	GGT	CGA	442
flu	Ser	Glu	Thr	Gln	Ile	Val	Ile	Leu	Glu	Lys	Ser	Asp	Ser	Gly	Arg	
		115					120					125				
TCG	TAT	GTT	TTC	CTT	CTT	CCG	ATC	GTT	GAG	GGA	CCG	TTC	CGA	ACC	TCG	490
Pro	Tyr	Val	Phe	Leu	Leu	Pro	Ile	Val	Glu	Gly	Pro	Phe	Arg	Thr	Ser	
ATT	CAG	CCT	GGG	GAT	GAT	GAC	TTT	GTC	GAT	GTT	TGT	GTC	GAG	AGT	GGT	538
ile	Gln	Pro	Gly	Asp	Asp	Asp	Phe	Val	Asp	Val	Cys	Val	Glu	Ser	Gly	
				150					155					160		
TCG	TCG	AAA	GTT	GTT	GAT	GCA	TCG	TTC	CGA	AGT	ATG	TTG	TAT	CTT	CAT	586
Ser	Ser	Lys	Val	Val	Asp	Ala	Ser	Phe	Arg	Ser	Met	Leu	Tyr	Leu	His	
				165					170					175		
GGT	GAT	GAT	CCG	TTT	GCA	CTT	GTT	AAA	GAG	GCG	ATG	AAG	ATC	GTG		634
ala	Gly	Asp	Asp	Pro	Phe	Ala	Leu	Val	Lys	Glu	Ala	Met	Lys	Ile	Val	
				180					185					190		
AGG	ACC	CAT	CTT	GGA	ACT	TTT	CGC	TTG	TTG	GAG	GAG	AAG	ACT	CCA	CCA	682
Arg	Thr	His	Leu	Gly	Thr	Phe	Arg	Leu	Leu	Glu	Glu	Lys	Thr	Pro	Pro	
GGT	ATC	GTG	GAC	AAA	TTC	GGT	TGG	TGC	ACG	TGG	GAC	GCG	TTT	TAC	CTA	730
Gly	Ile	Val	Asp	Lys	Phe	Gly	Trp	Cys	Thr	Trp	Asp	Ala	Phe	Tyr	Leu	
ACG	GTT	CAT	CCA	CAG	GGC	GTA	ATA	GAA	GGC	GTG	AGG	CAT	CTC	GTC	GAC	778
Thr	Val	His	Pro	Gln	Gly	Val	Ile	Glu	Gly	Val	Arg	His	Leu	Val	Asp	
				230					235					240		
GGC	GGT	TGT	CCT	CCC	GGT	TTA	GTC	CTA	ATC	GAC	GAT	GGT	TGG	CAA	TCC	826
Gly	Gly	Cys	Pro	Pro	Gly	Leu	Val	Leu	Ile	Asp	Asp	Gly	Trp	Gln	Ser	
				245					250					255		
ATC	GGA	CAC	GAT	TCG	GAT	CCC	ATC	ACC	AAA	GAA	GGA	ATG	AAC	CAA	ACC	874
Ile	Gly	His	Asp	Ser	Asp	Pro	Ile	Thr	Lys	Glu	Gly	Met	Asn	Gln	Thr	
				260					265					270		
GTC	GCC	GGC	GAG	CAA	ATG	CCC	TGC	CGT	CTT	TTG	AAA	TTC	CAA	GAG	AAT	922
Val	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	Leu	Leu	Lys	Phe	Gln	Glu	Asn	
				275					280					285		
TAC	AAA	TTC	CGT	GAC	TAC	GTC	AAT	CCC	AAG	GCC	ACC	GGC	CCC	CGA	GCC	970
Tyr	Lys	Phe	Arg	Asp	Tyr	Val	Asn	Pro	Lys	Ala	Thr	Gly	Pro	Arg	Ala	
GGC	CAG	AAG	GGG	ATG	AAG	GCG	TTT	ATA	GAT	GAA	CTC	AAA	GGA	GAG	TTT	1018
Gly	Gln	Lys	Gly	Met	Lys	Ala	Phe	Ile	Asp	Glu	Leu	Lys	Gly	Glu	Phe	
				310					315					320		
AAG	ACT	GTG	GAG	CAT	GTT	TAT	GTT	TGG	CAT	GCT	TTG	TGT	GGA	TAT	TGG	1066
Lys	Thr	Val	Glu	His	Val	Tyr	Val	Trp	His	Ala	Leu	Cys	Gly	Tyr	Trp	
				325					330					335		
GGT	GGC	CTT	CGC	CCG	CAG	GTG	CCT	GGC	TTG	CCT	GAG	GCA	CGT	GTG	ATT	1114
Gly	Gly	Leu	Arg	Pro	Gln	Val	Pro	Gly	Leu	Pro	Glu	Ala	Arg	Val	Ile	
				340					345					350		

AG CCA GTG CTT TCA CCA GGG CTG CAG ATG ACG ATG GAG GAT TTG GCG	1162
ln Pro Val Leu Ser Pro Gly Leu Gln Met Thr Met Glu Asp Leu Ala	
355 360 365	
TG GAT AAG ATT GTT CTT CAT AAG GTC GGG CTG GTC CCG CCG GAG AAG	1210
al Asp Lys Ile Val Leu His Lys Val Gly Leu Val Pro Pro Glu Lys	
70 375 380 385	
CT GAG GAG ATG TAC GAA GGA CTT CAT GCT CAT TTG GAA AAA GTT GGG	1258
la Glu Glu Met Tyr Glu Gly Leu His Ala His Leu Glu Lys Val Gly	
390 395 400	
TC GAC GGT GTT AAG ATT GAC GTT ATC CAC CTA TTG GAG ATG TTG TGT	1306
le Asp Gly Val Lys Ile Asp Val Ile His Leu Leu Glu Met Leu Cys	
405 410 415	
AA GAC TAT GGA GGG AGA GTG GAT TTG GCA AAG GCA TAT TAC AAA GCA	1354
lu Asp Tyr Gly Gly Arg Val Asp Leu Ala Lys Ala Tyr Tyr Lys Ala	
420 425 430	
TG ACC AAA TCA ATA AAT AAA CAT TTT AAA GGA AAT GGA GTC ATT GCA	1402
let Thr Lys Ser Ile Asn Lys His Phe Lys Gly Asn Gly Val Ile Ala	
435 440 445	
GT ATG GAA CAT TGT AAC GAC TTC ATG TTC CTT GGC ACG GAA GCT ATC	1450
er Met Glu His Cys Asn Asp Phe Met Phe Leu Gly Thr Glu Ala Ile	
450 455 460 465	
CT CTT GGT CGT GTT GGT GAT GAC TTT TGG TGC ACG GAC CCC TCT GGT	1498
er Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr Asp Pro Ser Gly	
470 475 480	
SAT CCA AAC GGT ACG TTT TGG CTC CAA GGA TGT CAC ATG GTT CAT TGT	1546
asp Pro Asn Gly Thr Phe Trp Leu Gln Gly Cys His Met Val His Cys	
485 490 495	
BCC AAC GAC AGC TTG TGG ATG GGG AAC TTC ATC CAC CCT GAC TGG GAT	1594
ala Asn Asp Ser Leu Trp Met Gly Asn Phe Ile His Pro Asp Trp Asp	
500 505 510	
ATG TTC CAA TCC ACC CAC CCT TGT GCC GCC TTC CAT GCT GCC TCT CGA	1642
Met Phe Gln Ser Thr His Pro Cys Ala Ala Phe His Ala Ala Ser Arg	
515 520 525	
BCC ATC TCT GGT GGC CCG ATC TAT GTT AGT GAT TCT GTG GGA AAG CAT	1690
Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Lys His	
530 535 540 545	
AAC TTT GAT CTT CTG AAA AAA CTA GTG CTT CCT GAT GGA TCG ATC CTT	1738
Asn Phe Asp Leu Leu Lys Lys Leu Val Leu Pro Asp Gly Ser Ile Leu	
550 555 560	
CGA AGT GAG TAC TAT GCA CTC CCG ACT CGC GAT TGT TTG TTT GAA GAC	1786
Arg Ser Glu Tyr Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe Glu Asp	
565 570 575	
CCT TTG CAT AAT GGA GAA ACT ATG CTT AAG ATT TGG AAT CTC AAC AAG	1834
Pro Leu His Asn Gly Glu Thr Met Leu Lys Ile Trp Asn Leu Asn Lys	
580 585 590	
TTC ACT GGA GTG ATT GGT GCA TTC AAC TGC CAA GGA GGA GGA TGG TGT	1882
Phe Thr Gly Val Ile Gly Ala Phe Asn Cys Gln Gly Gly Gly Trp Cys	
595 600 605	
CGT GAG ACA CGC CGC AAC CAA TGC TTT TCA CAA TAC TCA AAA CGA GTG	1930

Arg	Glu	Thr	Arg	Arg	Asn	Gln	Cys	Phe	Ser	Gln	Tyr	Ser	Lys	Arg	Val		
10					615					620					625		
CA	TCC	AAA	ACT	AAC	CCA	AAA	GAC	ATA	GAA	TGG	CAC	AGT	GGA	GAA	AAC	1978	
hr	Ser	Lys	Thr	Asn	Pro	Lys	Asp	Ile	Glu	Trp	His	Ser	Gly	Glu	Asn		
				630					635					640			
CT	ATC	TCT	ATT	GAA	GGC	GTT	AAA	ACC	TTT	GCG	CTT	TAC	CTC	TAT	CAA	2026	
ro	Ile	Ser	Ile	Glu	Gly	Val	Lys	Thr	Phe	Ala	Leu	Tyr	Leu	Tyr	Gln		
			645					650						655			
CC	AAA	AAA	CTT	ATC	CTC	TCC	AAG	CCC	TCT	CAA	GAT	CTT	GAC	ATA	GCT	2074	
la	Lys	Lys	Leu	Ile	Leu	Ser	Lys	Pro	Ser	Gln	Asp	Leu	Asp	Ile	Ala		
		660					665					670					
TT	GAC	CCA	TTC	GAA	TTC	GAG	CTC	ATC	ACT	GTT	TCA	CCA	GTG	ACC	AAA	2122	
eu	Asp	Pro	Phe	Glu	Phe	Glu	Leu	Ile	Thr	Val	Ser	Pro	Val	Thr	Lys		
	675					680				685							
TC	ATC	CAA	ACT	TCT	CTA	CAC	TTT	GCC	CCA	ATT	GGG	CTG	GTG	AAC	ATG	2170	
eu	Ile	Gln	Thr	Ser	Leu	His	Phe	Ala	Pro	Ile	Gly	Leu	Val	Asn	Met		
90					695				700					705			
TT	AAC	ACT	AGT	GGA	GCC	ATC	CAA	TCT	GTG	GAC	TAT	GAC	GAT	GAC	CTA	2218	
eu	Asn	Thr	Ser	Gly	Ala	Ile	Gln	Ser	Val	Asp	Tyr	Asp	Asp	Asp	Leu		
			710					715						720			
GC	TCA	GTC	GAG	ATT	GGT	GTC	AAA	GGG	TGT	GGT	GAG	ATG	CGA	GTA	TTT	2266	
er	Ser	Val	Glu	Ile	Gly	Val	Lys	Gly	Cys	Gly	Glu	Met	Arg	Val	Phe		
		725					730						735				
CA	TCG	AAA	AAA	CCA	AGG	GCT	TGT	CGT	ATT	GAT	GGG	GAG	GAT	GTT	GGG	2314	
la	Ser	Lys	Lys	Pro	Arg	Ala	Cys	Arg	Ile	Asp	Gly	Glu	Asp	Val	Gly		
		740					745					750					
TC	AAG	TAT	GAT	CAG	GAC	CAA	ATG	GTG	GTG	GTT	CAA	GTG	CCA	TGG	CCA	2362	
he	Lys	Tyr	Asp	Gln	Asp	Gln	Met	Val	Val	Val	Gln	Val	Pro	Trp	Pro		
	755					760					765						
ATT	GAT	TCT	TCA	TCG	GGT	GGC	ATT	TCG	GTT	ATC	GAG	TAC	TTG	TTT		2407	
le	Asp	Ser	Ser	Ser	Gly	Gly	Ile	Ser	Val	Ile	Glu	Tyr	Leu	Phe			
770					775					780							
CAATTTTAT TTATGTAAGC TCAATGATTG TTGTTGTTGT CGCTGTTGTT GCTATCAATG																2467	
TATTTCTCTC CAAAAGAAAA TTATGTGTAA TTTGGAGAGT AATTAAGTGA																2517	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 784 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Pro	Ser	Phe	Lys	Asn	Gly	Gly	Ser	Asn	Val	Val	Ser	Phe	Asp
1				5					10					15	
Gly	Leu	Asn	Asp	Met	Ser	Ser	Pro	Phe	Ala	Ile	Asp	Gly	Ser	Asp	Phe
			20					25					30		
Thr	Val	Asn	Gly	His	Ser	Phe	Leu	Ser	Asp	Val	Pro	Glu	Asn	Ile	Val
		35					40					45			
Ala	Ser	Pro	Ser	Pro	Tyr	Thr	Ser	Ile	Asp	Lys	Ser	Pro	Val	Ser	Val

50	55	60
Gly Cys Phe Val Gly Phe Asp Ala Ser Glu Pro Asp Ser Arg His Val		
65	70	75
Val Ser Ile Gly Lys Leu Lys Asp Ile Arg Phe Met Ser Ile Phe Arg		80
	85	90
Phe Lys Val Trp Trp Thr Thr His Trp Val Gly Arg Asn Gly Gly Asp		95
	100	105
Leu Glu Ser Glu Thr Gln Ile Val Ile Leu Glu Lys Ser Asp Ser Gly		110
	115	120
Arg Pro Tyr Val Phe Leu Leu Pro Ile Val Glu Gly Pro Phe Arg Thr		125
	130	135
Ser Ile Gln Pro Gly Asp Asp Asp Phe Val Asp Val Cys Val Glu Ser		140
145	150	155
Gly Ser Ser Lys Val Val Asp Ala Ser Phe Arg Ser Met Leu Tyr Leu		160
	165	170
His Ala Gly Asp Asp Pro Phe Ala Leu Val Lys Glu Ala Met Lys Ile		175
	180	185
Val Arg Thr His Leu Gly Thr Phe Arg Leu Leu Glu Glu Lys Thr Pro		190
	195	200
Pro Gly Ile Val Asp Lys Phe Gly Trp Cys Thr Trp Asp Ala Phe Tyr		205
	210	215
Leu Thr Val His Pro Gln Gly Val Ile Glu Gly Val Arg His Leu Val		220
225	230	235
Asp Gly Gly Cys Pro Pro Gly Leu Val Leu Ile Asp Asp Gly Trp Gln		240
	245	250
Ser Ile Gly His Asp Ser Asp Pro Ile Thr Lys Glu Gly Met Asn Gln		255
	260	265
Thr Val Ala Gly Glu Gln Met Pro Cys Arg Leu Leu Lys Phe Gln Glu		270
	275	280
Asn Tyr Lys Phe Arg Asp Tyr Val Asn Pro Lys Ala Thr Gly Pro Arg		285
	290	295
Ala Gly Gln Lys Gly Met Lys Ala Phe Ile Asp Glu Leu Lys Gly Glu		300
305	310	315
Phe Lys Thr Val Glu His Val Tyr Val Trp His Ala Leu Cys Gly Tyr		320
	325	330
Trp Gly Gly Leu Arg Pro Gln Val Pro Gly Leu Pro Glu Ala Arg Val		335
	340	345
Ile Gln Pro Val Leu Ser Pro Gly Leu Gln Met Thr Met Glu Asp Leu		350
	355	360
Ala Val Asp Lys Ile Val Leu His Lys Val Gly Leu Val Pro Pro Glu		365
	370	375
Lys Ala Glu Glu Met Tyr Glu Gly Leu His Ala His Leu Glu Lys Val		380
385	390	395
Gly Ile Asp Gly Val Lys Ile Asp Val Ile His Leu Leu Glu Met Leu		400
	405	410
Cys Glu Asp Tyr Gly Gly Arg Val Asp Leu Ala Lys Ala Tyr Tyr Lys		415
	420	425
Ala Met Thr Lys Ser Ile Asn Lys His Phe Lys Gly Asn Gly Val Ile		430
	435	440
		445

la	Ser	Met	Glu	His	Cys	Asn	Asp	Phe	Met	Phe	Leu	Gly	Thr	Glu	Ala
450						455					460				
le	Ser	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Cys	Thr	Asp	Pro	Ser
65					470					475					480
gly	Asp	Pro	Asn	Gly	Thr	Phe	Trp	Leu	Gln	Gly	Cys	His	Met	Val	His
				485					490						495
lys	Ala	Asn	Asp	Ser	Leu	Trp	Met	Gly	Asn	Phe	Ile	His	Pro	Asp	Trp
			500					505					510		
asp	Met	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Ala	Phe	His	Ala	Ala	Ser
		515					520					525			
arg	Ala	Ile	Ser	Gly	Gly	Pro	Ile	Tyr	Val	Ser	Asp	Ser	Val	Gly	Lys
		530				535					540				
his	Asn	Phe	Asp	Leu	Leu	Lys	Lys	Leu	Val	Leu	Pro	Asp	Gly	Ser	Ile
545					550					555					560
leu	Arg	Ser	Glu	Tyr	Tyr	Ala	Leu	Pro	Thr	Arg	Asp	Cys	Leu	Phe	Glu
				565					570					575	
asp	Pro	Leu	His	Asn	Gly	Glu	Thr	Met	Leu	Lys	Ile	Trp	Asn	Leu	Asn
			580					585					590		
lys	Phe	Thr	Gly	Val	Ile	Gly	Ala	Phe	Asn	Cys	Gln	Gly	Gly	Gly	Trp
		595					600					605			
cys	Arg	Glu	Thr	Arg	Arg	Asn	Gln	Cys	Phe	Ser	Gln	Tyr	Ser	Lys	Arg
	610					615					620				
val	Thr	Ser	Lys	Thr	Asn	Pro	Lys	Asp	Ile	Glu	Trp	His	Ser	Gly	Glu
525					630					635					640
asn	Pro	Ile	Ser	Ile	Glu	Gly	Val	Lys	Thr	Phe	Ala	Leu	Tyr	Leu	Tyr
				645					650					655	
gln	Ala	Lys	Lys	Leu	Ile	Leu	Ser	Lys	Pro	Ser	Gln	Asp	Leu	Asp	Ile
			660					665					670		
ala	Leu	Asp	Pro	Phe	Glu	Phe	Glu	Leu	Ile	Thr	Val	Ser	Pro	Val	Thr
		675					680					685			
lys	Leu	Ile	Gln	Thr	Ser	Leu	His	Phe	Ala	Pro	Ile	Gly	Leu	Val	Asn
	690					695					700				
met	Leu	Asn	Thr	Ser	Gly	Ala	Ile	Gln	Ser	Val	Asp	Tyr	Asp	Asp	Asp
705					710					715					720
leu	Ser	Ser	Val	Glu	Ile	Gly	Val	Lys	Gly	Cys	Gly	Glu	Met	Arg	Val
				725					730					735	
phe	Ala	Ser	Lys	Lys	Pro	Arg	Ala	Cys	Arg	Ile	Asp	Gly	Glu	Asp	Val
			740					745					750		
gly	Phe	Lys	Tyr	Asp	Gln	Asp	Gln	Met	Val	Val	Val	Gln	Val	Pro	Trp
		755					760					765			
pro	Ile	Asp	Ser	Ser	Ser	Gly	Gly	Ile	Ser	Val	Ile	Glu	Tyr	Leu	Phe
	770					775						780			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc= "Synthetic DNA"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
TYTAYCTBA CHGTNCAAYCC TCA

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2) INFORMATION FOR SEQ ID NO:7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc= "Synthetic DNA"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
TYTAYCTBA CHGTNCAAYCC CCA

23

2) INFORMATION FOR SEQ ID NO:8:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc= "Synthetic DNA"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
TYTAYCTBA CHGTNCAAYCC ACA

23

(2) INFORMATION FOR SEQ ID NO:9:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc= "Synthetic DNA"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
TTYTAYCTBA CHGTNCAAYCC GCA

23

(2) INFORMATION FOR SEQ ID NO:10:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc= "Synthetic DNA"
 (ix) FEATURE:
 (A) NAME/KEY:
 (B) LOCATION:

(D) OTHER INFORMATION: N at 6 and 11 = inosine
Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ARGGNGTNM GNCAICTRGT NGAYGG

26

2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: N at 6 and 11 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ARGGNGTNM GNCAICTYGT NGAYGG

26

2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: N at 6 and 11 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ARGGNGTNM GNCAITTRGT NGAYGG

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: N at 3 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

INGGNTGYT TYGTNGGYTT YGAYGC

26

2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: N at 3 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ITNGGNTGYT TYGTNGGRTT YGAYGC

26

2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: N at 9 and 11 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ITYGAYGCNT CNGARCCHGA YTCDCGNCA

29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: N at 9 and 11 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
TYGAYGCNT CNGARCCHGA YTCDAGYCA

30

2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc= "Synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AYCARGAYC TRATGGTNGT

20

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc= "Synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (D) OTHER INFORMATION: N at 6 and 15 = inosine
Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
CRTCACACG GRTGNCKNAC NCCYTC

26

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc= "Synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (D) OTHER INFORMATION: N at 6 and 15 = inosine
Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
CCRTCACACG GRTGNCKNAC NCCYTC

26

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc= "Synthetic DNA"
 (ix) FEATURE:
 (A) NAME/KEY:
 (B) LOCATION:
 (D) OTHER INFORMATION: N at 6 and 15 = inosine
 Other N = A, G, C, or T
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
 CRTCNACYA TRTGNCKNAC NCCYTC

26

2) INFORMATION FOR SEQ ID NO:21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc= "Synthetic DNA"
 (ix) FEATURE:
 (A) NAME/KEY:
 (B) LOCATION:
 (D) OTHER INFORMATION: N at 3 and 18 = inosine
 Other N = A, G, C, or T
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
 GNCGHGART CDGGYTCNGA NGCRTCRAA

29

2) INFORMATION FOR SEQ ID NO:22:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc= "Synthetic DNA"
 (ix) FEATURE:
 (A) NAME/KEY:
 (B) LOCATION:
 (D) OTHER INFORMATION: N at 19 = inosine
 Other N = A, G, C, or T
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
 RTGRCTHGAR TCDGGYTCNG ANGRTCRAA

30